Phyre^2

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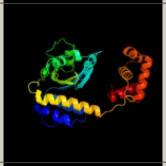
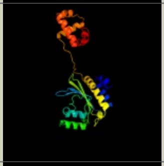
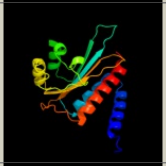
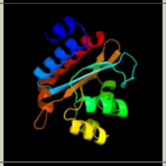
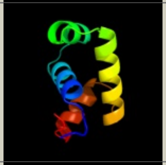
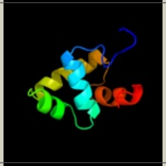
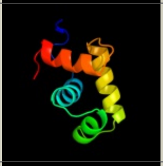
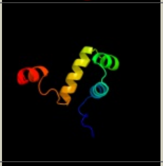
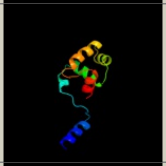
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1h0mD_	Alignment		100.0	19	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcriptional activator protein trar; **PDBTitle:** three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
2	c2q0oA_	Alignment		100.0	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
3	c3sztB_	Alignment		100.0	31	**PDB header:**transcription **Chain:** B: **PDB Molecule:**quorum-sensing control repressor; **PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
4	c3qp5C_	Alignment		100.0	26	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
5	c2avxA_	Alignment		100.0	99	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein sdia; **PDBTitle:** solution structure of e coli sdia1-171
6	d1l3la2	Alignment		99.8	16	**Fold:**Profilin-like **Superfamily:**Pheromone-binding domain of LuxR-like quorum-sensing transcription factors **Family:**Pheromone-binding domain of LuxR-like quorum-sensing transcription factors
7	c2uv0G_	Alignment		99.8	20	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcriptional activator protein lasr; **PDBTitle:** structure of the p. aeruginosa lasr ligand-binding domain2 bound to its autoinducer
8	c3qp1A_	Alignment		99.8	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir ligand-binding domain bound to the native2 ligand c6-hsl
9	c3cloC_	Alignment		99.8	41	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
10	c2krfB_	Alignment		99.7	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
11	d1l3la1	Alignment		99.7	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)

12	c1zljE_	Alignment		99.7	25	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
13	d1p4wa_	Alignment		99.7	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
14	d1fsea_	Alignment		99.7	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
15	d1a04a1	Alignment		99.7	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
16	c2rnjA_	Alignment		99.7	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
17	c3c3wB_	Alignment		99.7	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
18	c1x3uA_	Alignment		99.7	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein fixj; **PDBTitle:** solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
19	c3klnC_	Alignment		99.7	33	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** vibrio cholerae vpst
20	c1rnlA_	Alignment		99.6	31	**PDB header:**signal transduction protein **Chain:** A: **PDB Molecule:**nitrate/nitrite response regulator protein narl; **PDBTitle:** the nitrate/nitrite response regulator protein narl from narl
21	c2jpcA_	Alignment	not modelled	99.6	34	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
22	d1yioa1	Alignment	not modelled	99.6	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
23	c1zn2A_	Alignment	not modelled	99.6	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulatory protein; **PDBTitle:** low resolution structure of response regulator styr
24	d1ttya_	Alignment	not modelled	98.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
25	c1kgsA_	Alignment	not modelled	98.3	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna binding response regulator d; **PDBTitle:** crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
26	d2p7vb1	Alignment	not modelled	98.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
27	d1smyf2	Alignment	not modelled	98.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
28	d1rp3a2	Alignment	not modelled	98.2	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
						Fold:DNA/RNA-binding 3-helical bundle

29	d1xsva_	Alignment	not modelled	98.2	16	**Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
30	d1ku7a_	Alignment	not modelled	98.2	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
31	c2o8xA_	Alignment	not modelled	98.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
32	d1or7a1	Alignment	not modelled	98.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
33	c3hugA_	Alignment	not modelled	98.1	23	**PDB header:**transcription/membrane protein **Chain:** A: **PDB Molecule:**rna polymerase sigma factor; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
34	d1ku3a_	Alignment	not modelled	98.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
35	d1s7oa_	Alignment	not modelled	98.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
36	c3mzyA_	Alignment	not modelled	98.0	37	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna polymerase sigma-h factor; **PDBTitle:** the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
37	c3q9sA_	Alignment	not modelled	98.0	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra(1-215) from deinococcus radiodurans
38	c1rp3G_	Alignment	not modelled	98.0	23	**PDB header:**transcription **Chain:** G: **PDB Molecule:**rna polymerase sigma factor sigma-28 (flia); **PDBTitle:** cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm
39	c1or7A_	Alignment	not modelled	97.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma-e factor; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
40	c2q1zA_	Alignment	not modelled	97.7	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rpoe, ecf sige; **PDBTitle:** crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
41	c3t72o_	Alignment	not modelled	97.5	16	**PDB header:**transcription/dna **Chain:** O: **PDB Molecule:**pho box dna (strand 1); **PDBTitle:** phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
42	c2oqrA_	Alignment	not modelled	97.5	19	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
43	c1l9uH_	Alignment	not modelled	97.4	16	**PDB header:**transcription **Chain:** H: **PDB Molecule:**sigma factor siga; **PDBTitle:** thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
44	c2a6eF_	Alignment	not modelled	97.3	14	**PDB header:**transferase **Chain:** F: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** crystal structure of the t. thermophilus rna polymerase2 holoenzyme
45	d1jhfa1	Alignment	not modelled	97.2	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
46	c2hqrA_	Alignment	not modelled	97.1	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
47	d2cg4a1	Alignment	not modelled	97.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
48	c1ys7B_	Alignment	not modelled	96.9	25	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulatory protein prra; **PDBTitle:** crystal structure of the response regulator protein prra comlexed with2 mg2+
49	d1stza1	Alignment	not modelled	96.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
50	c2gwrA_	Alignment	not modelled	96.8	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dna-binding response regulator mtra; **PDBTitle:** crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
51	c3p7nB_	Alignment	not modelled	96.6	28	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
52	c3k2zA_	Alignment	not modelled	96.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
53	c1u78A_	Alignment	not modelled	96.5	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
						PDB header:antiviral protein

54	c2wteB_	Alignment	not modelled	96.4	27	**Chain:** B: **PDB Molecule:**csa3; **PDBTitle:** the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
55	c3r0jA_	Alignment	not modelled	96.4	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
56	d1biaa1	Alignment	not modelled	96.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
57	c2l4aA_	Alignment	not modelled	96.3	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
58	d2cyya1	Alignment	not modelled	96.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
59	d1i1ga1	Alignment	not modelled	96.3	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
60	d2d1ha1	Alignment	not modelled	96.3	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
61	d2cfxa1	Alignment	not modelled	96.3	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
62	c1p2fA_	Alignment	not modelled	96.1	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
63	c2cg4B_	Alignment	not modelled	96.1	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**regulatory protein asnc; **PDBTitle:** structure of e.coli asnc
64	c2e1cA_	Alignment	not modelled	96.1	19	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
65	d1j5ya1	Alignment	not modelled	96.1	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
66	c3iydF_	Alignment	not modelled	96.1	16	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
67	c2dbbA_	Alignment	not modelled	96.0	16	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
68	c2vbzA_	Alignment	not modelled	96.0	19	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
69	c2p6tH_	Alignment	not modelled	95.9	21	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
70	c2e7xA_	Alignment	not modelled	95.9	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
71	c1i1gA_	Alignment	not modelled	95.7	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
72	c3r0aB_	Alignment	not modelled	95.7	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
73	c2x4hA_	Alignment	not modelled	95.6	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
74	c2ewnA_	Alignment	not modelled	95.5	15	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
75	c2cfxD_	Alignment	not modelled	95.3	9	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
76	d2oola1	Alignment	not modelled	95.3	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
77	c2ia0A_	Alignment	not modelled	95.2	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator pf0864; **PDBTitle:** transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
78	c3cuoB_	Alignment	not modelled	95.2	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
79	c6paxA_	Alignment	not modelled	95.0	19	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6;

79	c6paxA_	Alignment	not modelled	95.0	19	**PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
80	c2fa5B_	Alignment	not modelled	95.0	7	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator marr/emrr family; **PDBTitle:** the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
81	c1b9nA_	Alignment	not modelled	94.9	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein (mode); **PDBTitle:** regulator from escherichia coli
82	d1r1ua_	Alignment	not modelled	94.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
83	d1sfxa_	Alignment	not modelled	94.9	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
84	d1r71a_	Alignment	not modelled	94.9	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
85	d1pdnc_	Alignment	not modelled	94.8	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
86	c2r0qF_	Alignment	not modelled	94.8	21	**PDB header:**recombination/dna **Chain:** F: **PDB Molecule:**putative transposon tn552 dna-invertase bin3; **PDBTitle:** crystal structure of a serine recombinase- dna regulatory2 complex
87	c1r71B_	Alignment	not modelled	94.7	28	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcriptional repressor protein korb; **PDBTitle:** crystal structure of the dna binding domain of korb in2 complex with the operator dna
88	c3tgnA_	Alignment	not modelled	94.7	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**adc operon repressor adcr; **PDBTitle:** crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
89	c3i4pA_	Alignment	not modelled	94.7	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, asnc family; **PDBTitle:** crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
90	c2vn2B_	Alignment	not modelled	94.7	17	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
91	d1r1ta_	Alignment	not modelled	94.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
92	d1lnwa_	Alignment	not modelled	94.6	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
93	d1okra_	Alignment	not modelled	94.6	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
94	d1k78a1	Alignment	not modelled	94.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
95	c2it0A_	Alignment	not modelled	94.5	30	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of a two-domain ider-dna complex crystal2 form ii
96	c1r22B_	Alignment	not modelled	94.4	15	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**transcriptional repressor smtb; **PDBTitle:** crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
97	c2gm4B_	Alignment	not modelled	94.4	19	**PDB header:**recombination, dna **Chain:** B: **PDB Molecule:**transposon gamma-delta resolvase; **PDBTitle:** an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
98	d1gxqa_	Alignment	not modelled	94.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
99	c2oqgA_	Alignment	not modelled	94.4	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
100	c3frwF_	Alignment	not modelled	94.4	19	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
101	d2o9ca1	Alignment	not modelled	94.3	8	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
102	c2zxjB_	Alignment	not modelled	94.3	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein walr; **PDBTitle:** crystal structure of yycf dna-binding domain from staphylococcus2 aureus
103	d1vz0a1	Alignment	not modelled	94.2	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
104	d6paxa1	Alignment	not modelled	94.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
						PDB header:transcription

105	c2hwvA_	Alignment	not modelled	94.2	23	**Chain:** A: **PDB Molecule:**dna-binding response regulator vicr; **PDBTitle:** crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
106	c3korD_	Alignment	not modelled	94.0	22	**PDB header:**transcription **Chain:** D: **PDB Molecule:**possible trp repressor; **PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus
107	c2x48B_	Alignment	not modelled	94.0	28	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
108	c3trcA_	Alignment	not modelled	93.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii
109	c2v79B_	Alignment	not modelled	93.9	19	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
110	c3f6oB_	Alignment	not modelled	93.9	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
111	d2p4wa1	Alignment	not modelled	93.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF1790-like
112	c3nqoB_	Alignment	not modelled	93.8	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**marr-family transcriptional regulator; **PDBTitle:** crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
113	c2elhA_	Alignment	not modelled	93.8	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
114	c1f5tA_	Alignment	not modelled	93.8	33	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
115	d3broa1	Alignment	not modelled	93.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
116	d2a61a1	Alignment	not modelled	93.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
117	c2nyxB_	Alignment	not modelled	93.6	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis
118	d2g9wa1	Alignment	not modelled	93.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
119	c2nnnB_	Alignment	not modelled	93.5	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
120	d1kgsa1	Alignment	not modelled	93.4	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like